FIG. 1

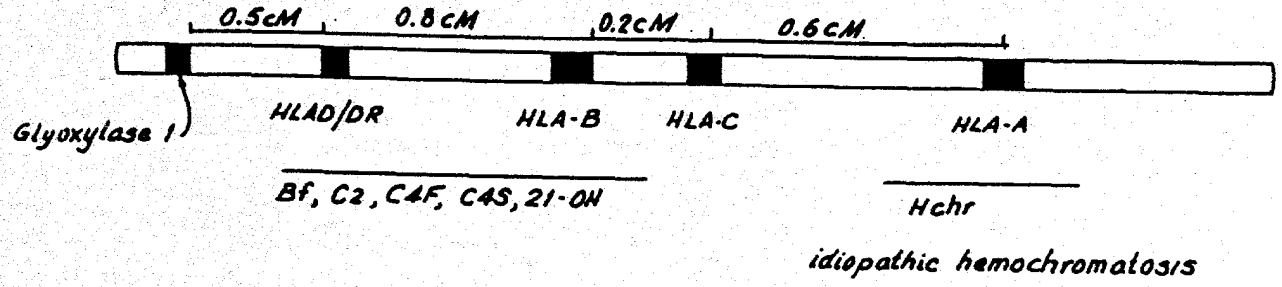
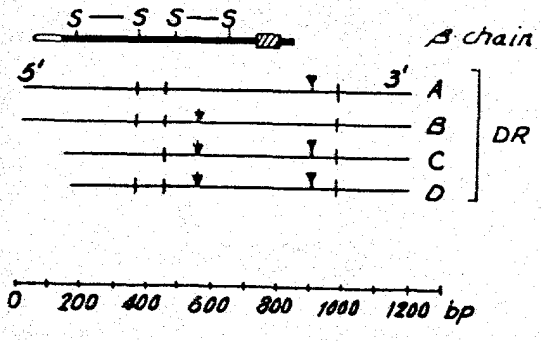


FIG. 4



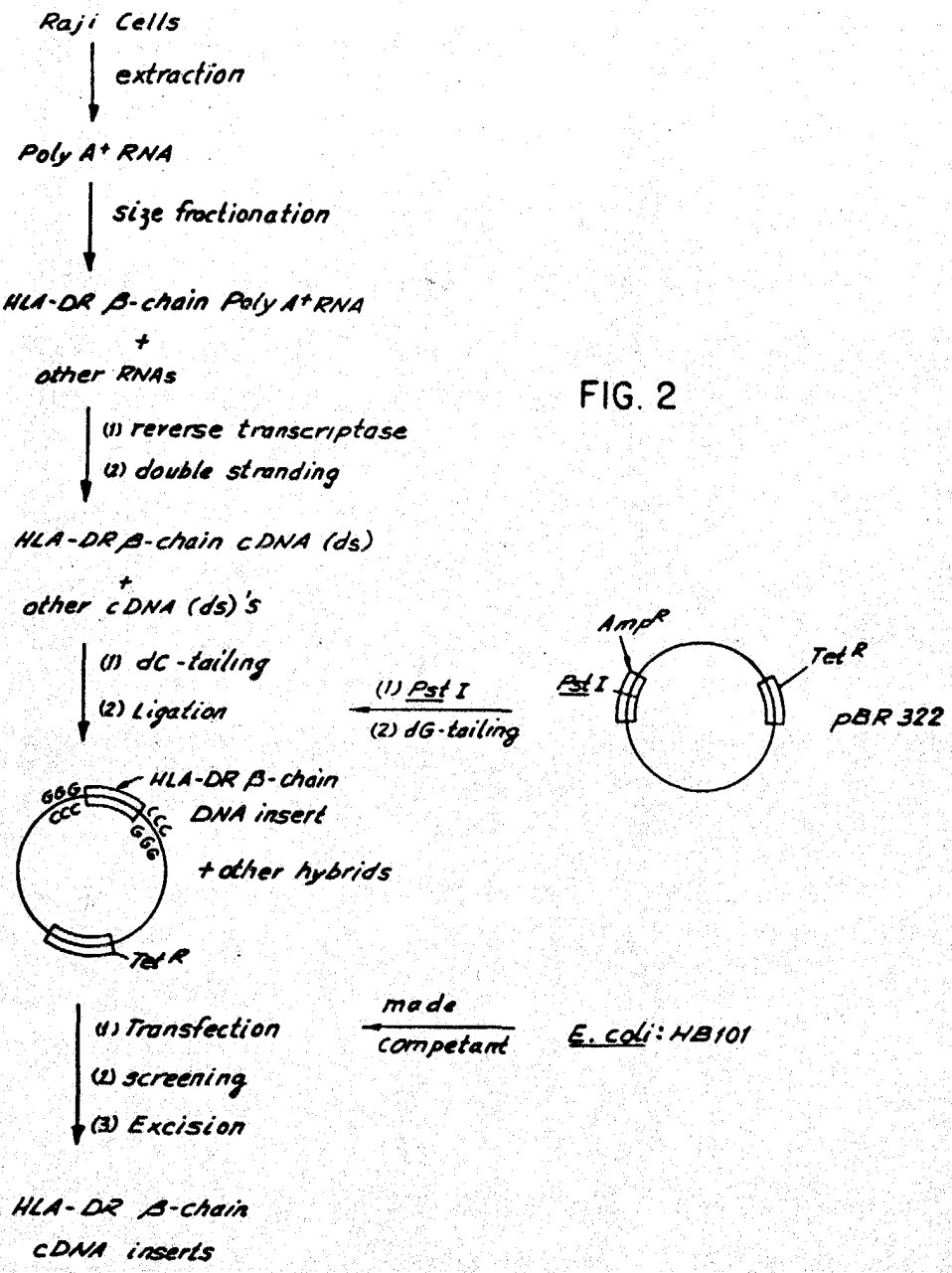

Raji Cells
extraction
Poly A+ RNA
size fractionation
HLA-DR β-chain Poly A+ RNA
+
other RNAs
(1) reverse transcriptase
(2) double stranding
HLA-DR β-chain cDNA (ds)
+
other cDNA (ds)'s
(1) dC-tailing
(2) Ligation
(1) Pst I
(2) dG-tailing
Amp R
Pst I
Tet R
pBR 322
GGG
CCC
CCC
GGG
HLA-DR β-chain
DNA insert
+other hybrids
Tet R
(1) Transfection
(2) screening
(3) Excision
made
competant
E. coli: HB101
HLA-DR β-chain
cDNA inserts

FIG. 2

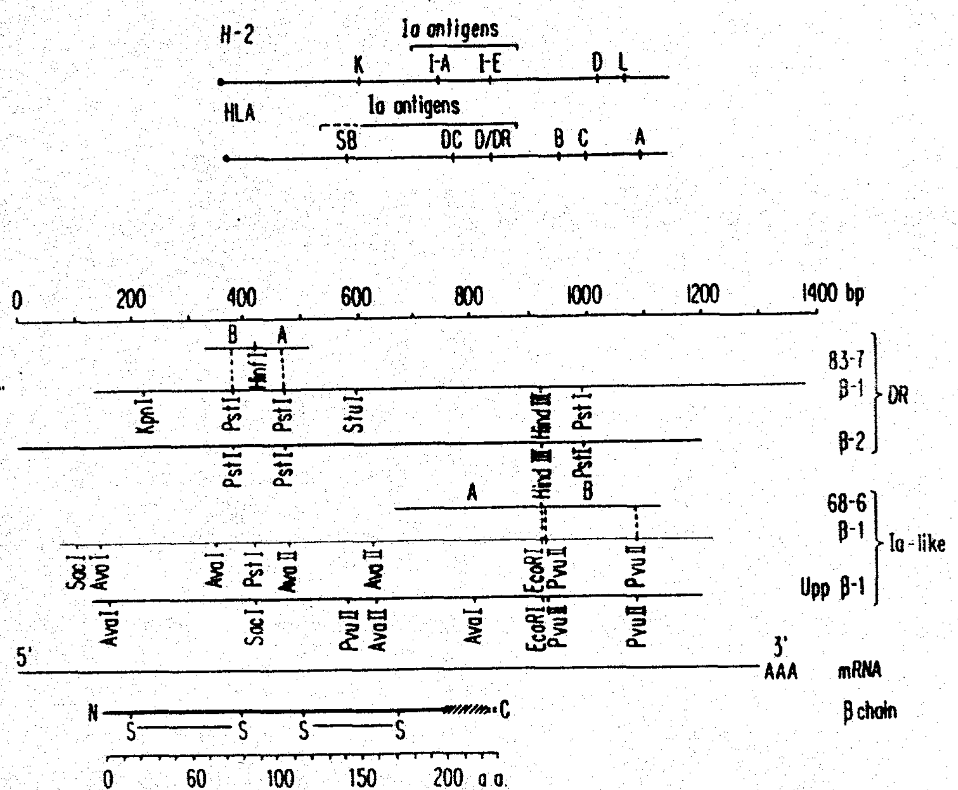


FIG. 3

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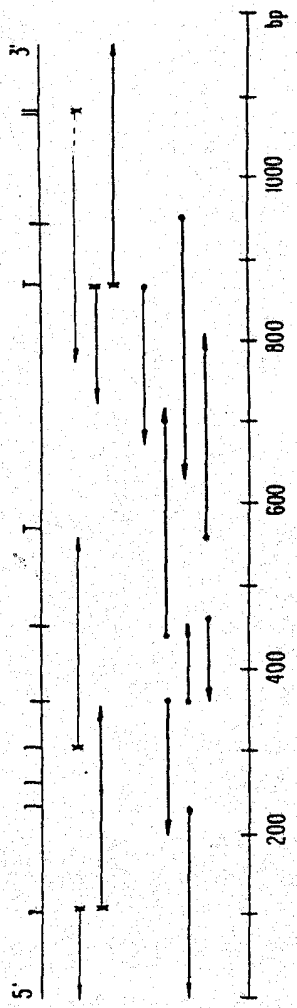
FIG. 5



```
                                                        -29
                                                         M   V   C   L
(G)n CTCCTCTGGCCCCTGGTCCTGTCCTCTTCTCCAGC ATG GTG TGT CTG      47

 K   L   P   G   G   S   S   L   A   A   L   T   V   T
AAG CTC CCT GGA GGC TCC AGC TTG GCA GCG TTG ACA GTG ACA      89

                                                    1
 L   M   V   L   S   S   R   L   A   F   A   G   D   T
CTG ATG GTG CTG AGC TCC CGA CTG GCT TTC GCT GGG GAC ACC     131

                                10
 R   P   R   F   L   E   L   L   K   S   E   C   H   F
CGA CCA CGT TTC TTG GAG CTG CTT AAG TCT GAG TGT CAT TTC     173

             20                                         30
 F   N   G   T   E   R   V   R   F   L   E   R   H   F
TTC AAT GGG ACG GAG CGG GTG CGG TTC CTG GAG AGA CAC TTC     215

                                        40
 H   N   Q   E   E   Y   A   R   F   D   S   D   V   G
CAT AAC CAG GAG GAG TAC GCG CGC TTC GAC AGC GAC GTG GGG     257
```

FIG. 5A

```
                        50
 E   Y   R   A   V   R   E   L   G   R   P   D   A   E
GAG TAC CGG GCG GTG AGG GAG CTG GGG CGG CCT GAT GCC GAG      299

 60                                                  70
 Y   W   N   S   Q   K   D   L   L   E   Q   K   R   G
TAC TGG AAC AGC CAG AAG GAC CTC CTG GAG CAG AAG CGG GGC      341

                            80
 Q   V   D   N   Y   C   R   H   N   Y   G   V   V   E
CAG GTG GAC AAT TAC TGC AGA CAC AAC TAC GGG GTT GTG GAG      383

             90                                         100
 S   F   T   V   Q   R   R   V   H   P   Q   V   T   V
AGC TTC ACA GTG CAG CGG CGA GTC CAT CCT CAG GTG ACT GTG      425

                                    110
 Y   P   A   K   T   Q   P   L   Q   H   H   N   L   L
TAT CCT GCA AAG ACC CAG CCC CTG CAG CAC CAC AAC CTC CTG      467

                    120
 V   C   S   V   S   G   F   Y   P   G   S   I   E   V
GTC TGC TCT GTG AGT GGT TTC TAT CCA GGC AGC ATT GAA GTC      509
```

FIG. 5B

```
130                                                 140
 R   W   F   R   N   G   Q   E   E   K   A   G   V   V
AGG TGG TTC CGG AAC GGC CAG GAA GAG AAG GCT GGG GTG GTG      551

                            150
 S   T   G   L   I   Q   N   G   D   W   T   F   Q   T
TCC ACG GGC CTG ATC CAG AAT GGA GAC TGG ACC TTC CAG ACC      593

        160                                         170
 L   V   M   L   E   T   F   P   R   S   G   E   V   Y
CTG GTG ATG CTA GAA ACA TTT CCT CGG AGT GGA GAG GTT TAC      635

                                    180
 T   C   Q   V   E   H   P   S   V   T   S   P   L   T
ACC TGC CAA GTG GAG CAC CCA AGC GTA ACG AGC CCT CTC ACA      677

                    190
 V   E   W   S   A   R   S   E   S   A   Q   S   K   M
GTG GAA TGG AGT GCA CGG TCT GAA TCT GCA CAG AGC AAG ATG      719

200                                                 210
 L   S   G   V   G   G   F   V   L   G   L   L   F   L
CTG AGT GGA GTC GGG GGC TTT GTG CTG GGC CTG CTC TTC CTT      761
```

FIG. 5C

```
                                220
 G   A   G   L   F   I   Y   F   R   N   Q   K   G   H
GGG GCC GGG CTG TTC ATC TAC TTC AGG AAT CAG AAA GGA CAC      803

        230                             237
 S   G   L   Q   P   T   G   F   L   S
TCT GGA CTT CAG CCA ACA GGA TTC CTG AGC TGA AGTGCAGATGA      847

CAATTTAAGGAAGAATCTTCTTCCCCAGCTTTGCAGGATGAAAAGCTTTCCCGCC     902

TGGCTGTTATTCTTCCACGAGAGAGGGCTTTCTCAGGACCTAGTTGCTACTGGTT     957

CAGCAACTGCAGAAAATGTCCTCCCTTGTGGCTTCCTCAGTTCCTGCCCTTGGCC    1012

TGAAGTCCCAGCATTGATGGCAGCGCCTCATCTTCAACTTTTGTGCTCCCCTTTG    1067

CCTAAACCCTATGGCCTCCTGTGCATCTGTACTCACCCTGTACCACAAACACATT    1122

ACATTATTAAATGTTTCTCAAAGATGGAGTTAAAAAAA(C)n                 1160
```

FIG. 5D

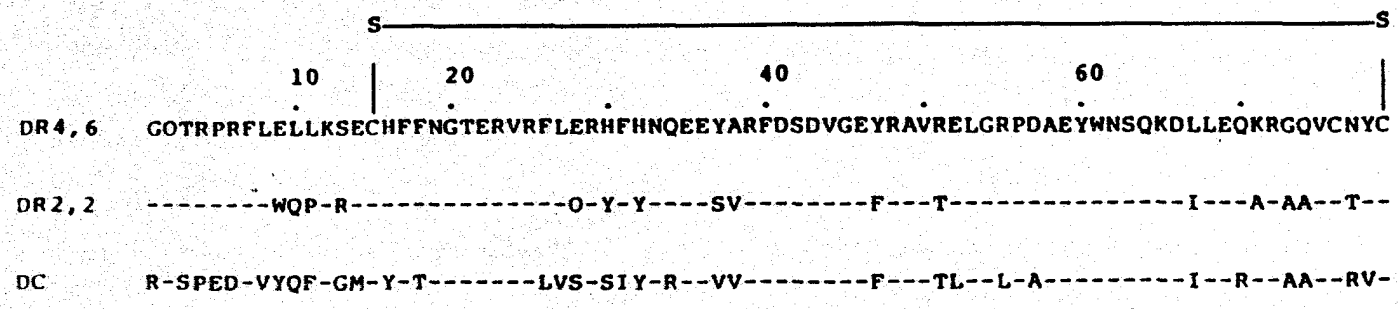


FIG. 6A

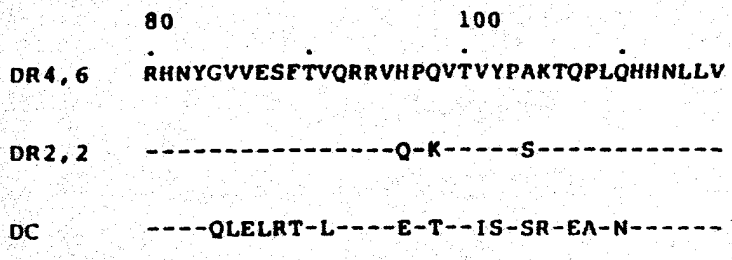


FIG. 6B

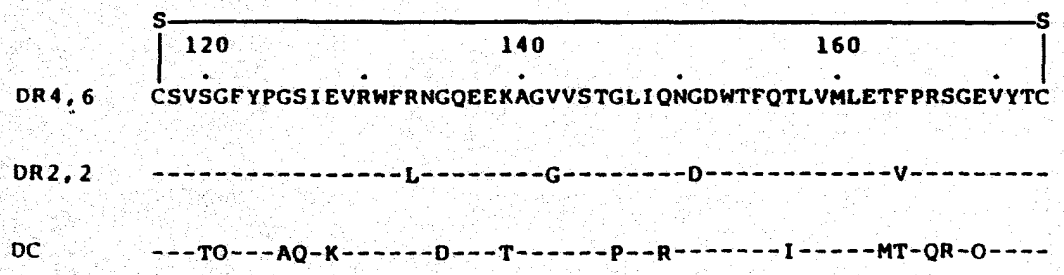


FIG. 6C

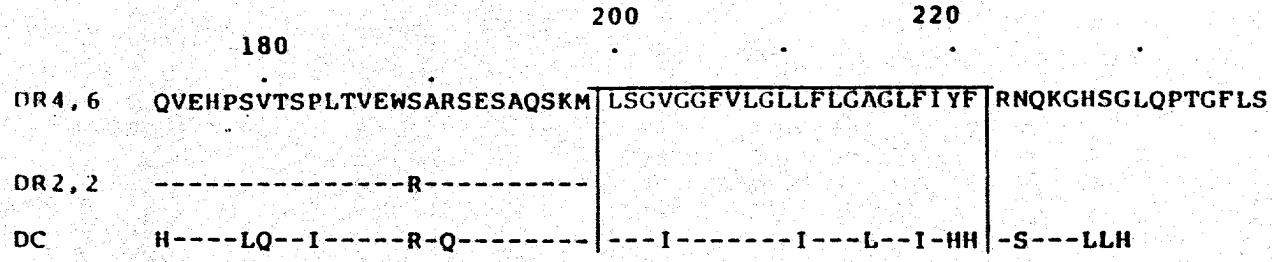

200
220
180
DR4,6 QVEHPSVTSPLTVEWSARSESAQSKM LSGVGGFVLGLLFLGAGLFIYF RNQKGHSGLQPTGFLS
DR2,2 ----------R----------
DC H----LQ--I-----R-Q--------|---I-------I---L--I-HH|-S---LLH

FIG. 6D

FIG. 7

```
                                                                                  M   V   C   L   K   F   P   G
A GTT CTC CCT GAG TGA GAC TCA CCT GCT CCT CTG GCC CCT GGT CCT GTC CTG TTC TCC AGC ATG GTG TGT CTG AAG TTC CCT GGA   85

                                                                               -1   1
G   S   C   M   A   A   L   T   V   T   L   M   V   L   S   S   P   L   A   L   A   G   D   T   R   P   R   F   L
GGC TCC TGC ATG GCA GCT CTG ACA GTG ACA CTG ATG GTG CTG AGC TCC CCA CTG GCT TTG GCT GGG GAC ACC CGA CCA CGT TTC TTG   172

    10                                      20                                      30
E   Q   V   K   H   E   C   H   F   F   N   G   T   E   R   V   R   F   L   D   R   Y   F   Y   H   Q   E   E   Y
GAG CAG GTT AAA CAT GAG TGT CAT TTC TTC AAC GGG ACG GAG CGG GTG CGG TTC CTG GAC AGA TAC TTC TAT CAC CAA GAG GAG TAC   259

        40                                      50                                      60
V   R   F   D   S   D   V   G   E   Y   R   A   V   T   E   L   G   R   P   D   A   E   Y   W   N   S   Q   K   D
GTG CGC TTC GAC AGC GAC GTG GGG GAG TAC CGG GCG GTG ACG GAG CTG GGG CGG CCT GAT GCC GAG TAC TGG AAC AGC CAG AAG GAC   346

            70                                      80                                      90
L   L   E   Q   K   R   A   A   V   D   T   Y   C   R   H   N   Y   G   V   G   E   S   F   T   V   Q   R   R   V
CTC CTG GAG CAG AAG CGG GCC GCG GTG GAC ACC TAC TGC AGA CAC AAC TAC GGG CTT GGT GAG AGC TTC ACA GTG CAG CGG CGA GTC   433

                100                                     110                                     120
Y   P   E   V   T   V   Y   P   A   K   T   Q   P   L   Q   H   H   N   L   L   V   C   S   V   N   G   F   Y   P
TAT CCT GAG GTG ACT GTG TAT CCT GCA AAG ACC CAG CCC CTG CAG CAC CAC AAC CTC CTG GTC TGC TCT GTG AAT GGT TTC TAT CCA   520

                    130                                     140                                     150
G   S   I   E   V   R   W   F   R   N   G   Q   E   E   K   T   G   V   V   S   T   G   L   I   Q   N   G   D   W
GGC AGC ATT GAA GTC AGG TGG TTC CGG AAC GGC CAG GAA GAG AAG ACT GGG GTG GTG TCC ACA GGC CTG ATC CAG AAT GGA GAC TGG   607
```

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FIG. 7A

```
                         160                                           170                                           180
 T   F   Q   T   L   V   M   L   E   T   V   P   R   S   G   E   V   Y   T   C   Q   V   E   H   P   S   L   T   S
ACC TTC CAG ACC CTG GTG ATG CTG GAA ACA GTT CCT CGG AGT GGA GAG GTT TAC ACC TGC CAA GTG GAG CAC CCA AGC CTG ACG AGC   694

                             190                                           200                                           210
 P   L   T   V   E   W   R   A   R   S   E   S   A   Q   S   K   M   L   S   G   V   G   G   F   V   L   G   L   L
CCT CTC ACA GTG GAA TGG AGA GCA CGG TCT GAA TCT GCA CAG AGC AAG ATG CTG AGT GGA GTC GGG GGC TTC GTG CTG GGC CTG CTC   781

                                 220                                         230                             237
 F   L   G   A   G   L   F   I   Y   F   R   N   Q   K   G   H   S   G   L   Q   P   T   G   F   L   S
TTC CTT GGG GCC GGG CTG TTC ATC TAC TTG AGG AAT CAG AAA GGA CAC TCT GGA CTT CAG CCA ACA GGA TTC CTG AGC TGA AGT GAA   868

GAT GAC CAC ATT CAA GGA AGA ACC TTC TGC CCC AGC TTT GCA GGA TGA AAC ACT TCC CCG CTT GGC TCT CAT TCT TCC ACA AGA GAG   955

ACC TTT CTC CGG ACC TGG TTG CTA CTG GTT CAG CAG CTC TGC AGA AAA TGT CCT CCC TTG TGG CTG CCT CAG CTC GTA CCT TTG GCC  1042

TGA AGT CCC AGC ATT AAT GGC AGC CCC TCA TCT TCC AAG TTT TGT GCT CCC CTT TAC CTA ATG CTT CCT GCG TCC CAT GCA TCT GTA  1129

CTC CTG CTG TGC CAC AAA CAC ATT ACA TTA TTA AAT GTT TCT CAA ACA TGG AGT TAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AA   1215
```

FIG. 8

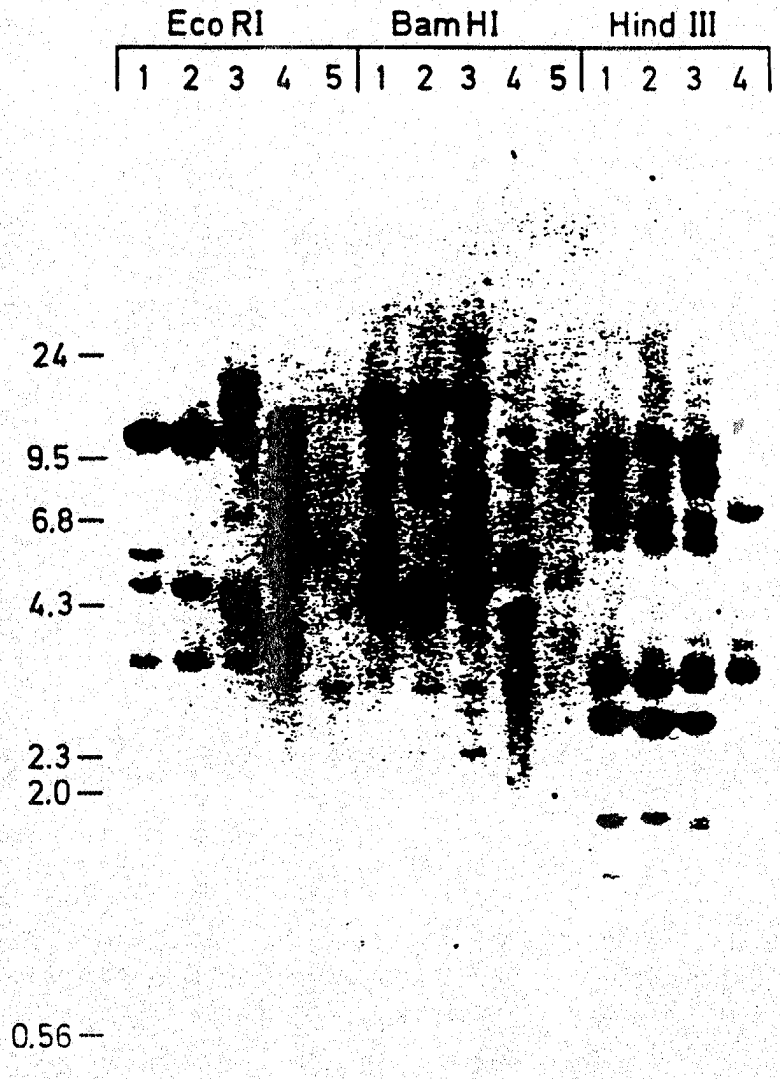
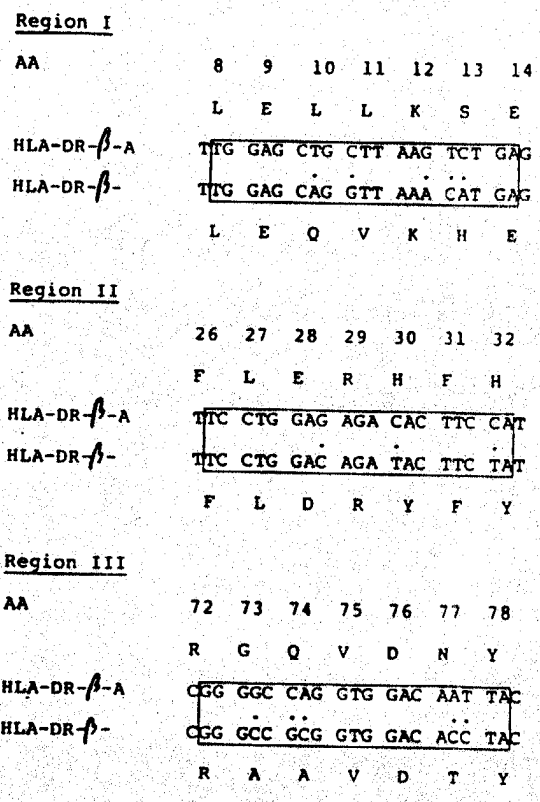


FIG. 9


Region I
AA
8 9 10 11 12 13 14
L E L L K S E
HLA-DR-β-A
TTG GAG CTG CTT AAG TCT GAG
HLA-DR-β-
TTG GAG CAG GTT AAA CAT GAG
L E Q V K H E
Region II
AA
26 27 28 29 30 31 32
F L E R H F H
HLA-DR-β-A
TTC CTG GAG AGA CAC TTC CAT
HLA-DR-β-
TTC CTG GAC AGA TAC TTC TAT
F L D R Y F Y
Region III
AA
72 73 74 75 76 77 78
R G Q V D N Y
HLA-DR-β-A
CGG GGC CAG GTG GAC AAT TAC
HLA-DR-β-
CGG GCC GCG GTG GAC ACC TAC
R A A V D T Y